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PCT09

## RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/720,583A

TIME: 13:24:11

Input Set : A:\MBHB00-1314 SequenceListing.txt

Output Set: N:\CRF3\12212001\I720583A.raw

ENTERED

3 <110> APPLICANT: DSM N.V.  
 4 POUWELS, Pieter  
 5 van LUIJK, Nicole  
 6 JORE, Johannes  
 7 LUITEN, Rudolf  
 9 <120> TITLE OF INVENTION: Propionibacterium Vector  
 11 <130> FILE REFERENCE: MBHB00-1314  
 13 <140> CURRENT APPLICATION NUMBER: US 09/720,583A  
 14 <141> CURRENT FILING DATE: 2000-12-22  
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/04416  
 17 <151> PRIOR FILING DATE: 1999-06-25  
 19 <150> PRIOR APPLICATION NUMBER: EP 98305033.7  
 20 <151> PRIOR FILING DATE: 1998-06-25  
 22 <160> NUMBER OF SEQ ID NOS: 13  
 24 <170> SOFTWARE: PatentIn version 3.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 3555  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Propionibacterium freudenreichii LMG16545  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (273)..(1184)  
 36 <400> SEQUENCE: 1  
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 39 gcccataatgc ccgaacacgc cccagccatc ccttggagca ggtggcagcg tcaggggagt 120  
 41 cgggggatgt ttggcagggg atgtggaaag agagttcgct ttgctcacat ggctcaaccg 180  
 43 ggtaactaac tgatatgggg tcttcgtcgc ccacttgaa cacgccgagg aatggaccac 240  
 45 gctgaacgtg actcgcatgc ttcaactgtcat gt atg gat tgc ttc gag acg ttg 293  
 46 Met Asp Ser Phe Glu Thr Leu  
 47 1 5  
 49 ttc cct gag agc tgg ctg cca cgc aag ccg ctg gcg tca gcc gag aag 341  
 50 Phe Pro Glu Ser Trp Leu Pro Arg Lys Pro Leu Ala Ser Ala Glu Lys  
 51 10 15 20  
 53 tct ggg gcg tac cgg cac gtg act ccg cag agg gcg ctg gag ctg cct 389  
 54 Ser Gly Ala Tyr Arg His Val Thr Arg Gln Arg Ala Leu Glu Leu Pro  
 55 25 30 35  
 57 tac atc gaa gcg aac ccg ttg gtc atg cag tcc ttg gtc atc acc gat 437  
 58 Tyr Ile Glu Ala Asn Pro Leu Val Met Gln Ser Leu Val Ile Thr Asp  
 59 40 45 50 55  
 61 cga gat gct tcg gat gct gac tgg gcc gca gac ctc gct ggg ctg cct 485  
 62 Arg Asp Ala Ser Asp Ala Asp Trp Ala Ala Asp Leu Ala Gly Leu Pro  
 63 60 65 70  
 65 tca ccg tcc tac gtg tcc atg aac cgt gtc acg acc acc gga cac atc 533  
 66 Ser Pro Ser Tyr Val Ser Met Asn Arg Val Thr Thr Gly His Ile  
 67 75 80 85  
 69 gtc tat gcc ttg aag aac cct gtg tgt ctg acc gat gcc gcg cgg cga 581  
 70 Val Tyr Ala Leu Lys Asn Pro Val Cys Leu Thr Asp Ala Ala Arg Arg

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71	90	95	100	
73	cgg cct atc aac ctg ctc gcc cgc gtc gag cag ggc cta tgc gac gtt			629
74	Arg Pro Ile Asn Leu Ileu Ala Arg Val Glu Gln Gly Leu Cys Asp Val			
75	105	110	115	
77	ctc ggc gat gca tcc tac ggg cac cgg atc aca aag aac ccg ctc			677
78	Leu Gly Gly Asp Ala Ser Tyr Gly His Arg Ile Thr Lys Asn Pro Leu			
79	120	125	130	135
81	agc acc gcc cat gcg acc ctc tgg ggc ccc gca gac gcg ctc tac gag			725
82	Ser Thr Ala His Ala Thr Leu Trp Gly Pro Ala Asp Ala Leu Tyr Glu			
83	140	145	150	
85	ctg cgc gcc ctc gca cac acc ctc gac gag atc cac gca ctg ccg gag			773
86	Leu Arg Ala Leu Ala His Thr Leu Asp Glu Ile His Ala Leu Pro Glu			
87	155	160	165	
89	gca ggg aac ccg cgt cgc aac gtc acc cga tca acg gtc ggc cgc aac			821
90	Ala Gly Asn Pro Arg Arg Asn Val Thr Arg Ser Thr Val Gly Arg Asn			
91	170	175	180	
93	gtc acc ctg ttc gac acc ccg atg tgg gca tac cgg gcc gtc ccg			869
94	Val Thr Leu Phe Asp Thr Thr Arg Met Trp Ala Tyr Arg Ala Val Arg			
95	185	190	195	
97	cac tcc tgg ggc ggc ccg gtc gcc gaa tgg gag cac acc gta ttc gag			917
98	His Ser Trp Gly Gly Pro Val Ala Glu Trp Glu His Thr Val Phe Glu			
99	200	205	210	215
101	cac atc cac cta ctg aac gag acg atc atc gcc gac gaa ttc gcc aca			965
102	His Ile His Leu Leu Asn Glu Thr Ile Ile Ala Asp Glu Phe Ala Thr			
103	220	225	230	
105	ggc ccc ctc ggc ttg aac gaa ctt aag cac tta tct cga tcc att tcc			1013
106	Gly Pro Leu Gly Leu Asn Glu Leu Lys His Leu Ser Arg Ser Ile Ser			
107	235	240	245	
109	cga tgg gtc tgg cgc aac ttc acc ccc gaa acc ttc cgc gca cgc cag			1061
110	Arg Trp Val Trp Arg Asn Phe Thr Pro Glu Thr Phe Arg Ala Arg Gln			
111	250	255	260	
113	aaa gcg atc agc ctc cgt gga gca tcc aaa ggc ggc aaa gaa ggc ggc			1109
114	Lys Ala Ile Ser Leu Arg Gly Ala Ser Lys Gly Gly Lys Glu Gly Gly			
115	265	270	275	
117	cac aaa ggc ggc att gcc agt ggc gca tca cgg cgc gcc cat acc cgt			1157
118	His Lys Gly Gly Ile Ala Ser Gly Ala Ser Arg Arg Ala His Thr Arg			
119	280	285	290	295
121	caa cag ttc ttg gag ggt ctc tca tga ccacacgtga acgtctcccc			1204
122	Gln Gln Phe Leu Glu Gly Leu Ser			
123	300			
125	cgcacggct acagcatcgc cgctgctgcg aaaaagctcg gtgtctccga gtccaccgtc			1264
127	aagggtggta cttccgagcc acgcgaggag ttctggccc gcgttgcgc acgccacgc			1324
129	cggattcggt agctccgctc ggagggtcag agcatcgctg cgattgtgc cgaggtcggt			1384
131	gtttccgtgg gcacccgtca ctacgcgcgt aacaagaatc gaactgacgc atgaccgtaa			1444
133	cgcgcacga tgagcatttt ctgtatcgta caccgcttgg cactacgttc gcgtgcgggtt			1504
135	gcacagtgcg cgccacgttc ttatcctgcg gccattgtgg ctacagccaa tggggggcat			1564
137	cagcaacgga cgttgaaacc ggtggcaag tgttactcag ggggacatgc ccagtctgcg			1624
139	gcgctcgat tgacgtatg gcagtcgtc atgcggccccc accgtcaac tcattcaggt			1684
141	atcgtgaga accctcatgg caccctctcg tgacacgttc tcgttgcgt cagctgctgt			1744

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143 gctgcgggc gtgagcgttt ctacgctgcg gcgcaggaaa tcagagcttg aggctccgg 1804  
 145 agcgcggta gaccgtccg gttgggttgt gccactgcgt gcactcaagg tcgtttttgg 1864  
 147 ggttcagat gagacctcga atgcggccgg tcatgacgt gagtttagtgg cgcaagtcgc 1924  
 149 ctctgagaac gagttttac ggcgtcaggt cgaggcagcag gcgcgcacga tcgaacggca 1984  
 151 ggctgaggca cacgcgggtgg tctcagcgcg gtcacacgg gttggccagc ttgaggccgg 2044  
 153 cgacgcagca gcaccgacac tggcacccgt tgaaaggccg gctccgcac ggcgggtgg 2104  
 155 gcagcgtcgg tagcgtcag gatcgtctg gcgtgacgag tgtgtctggc agtgcgaaca 2164  
 157 gttgctcgac cagtggcagc agaagcgaga tcgctgcgtg gtgtgttcc tcggtcagg 2224  
 159 cgtcgaggac tggcggtct tgctgcgtcc agccgategc ctcggcgccc aagtcagg 2284  
 161 ccaagctgtg ccaacgcaca cgcggctcgg ctgacagctg agtctcgaac tgcactgt 2344  
 163 gaccggccgg aagatgcacg ttgcccgggt cgtgagtggc caagcgacg tcaaagagtg 2404  
 165 ctgcttcgta gccgcgcaga aatggcagtg ctcggtcgat tcggatccgc ctggcccggt 2464  
 167 acattccggg ccgcttgatg aacgcctccg cgtagaagcg caccgttctc ggcccgccct 2524  
 169 cgtgatctgt cactgtgcac gtcctctcg atggttctcg acgttacccg agaccaccga 2584  
 171 cgttcatgcc cagcgcagcg acctgaaagg accaagccga gttagccgtg ctaaccgtat 2644  
 173 agttgttcc gtcgcctctg agggcaacca ctcgcgcagc aggtggccgg cagccgcgc 2704  
 175 gcaagcgcct accgggtttg ggcacagccc ataaatcaac gcctccgggt ttgaagcgat 2764  
 177 cgtgtgtcac gattgtatcg ctgtctaccc cttaggggtt ttcgtataaca caaatcaagt 2824  
 179 ttttcgtat acgctaattgc catgagtgag catctactgc acggcaagcc cgtcaccaac 2884  
 181 gagcagattc aggcatgggc agacgaggcc gaggccggat acgaccgtcc caaactcccc 2944  
 183 aagccacggc gcgacgcggc gcccgttaga gacgtccgg gcaccgtcgt acccggtcgt 3004  
 185 ctcgacgcgg ccaccgttgc cgctctcaca gaacgagcaa cagccgaggg catcacgaac 3064  
 187 cgttcagacg cgatccgagc cgcagttccac gagttggacac ggggtgcctg acctccacga 3124  
 189 ctcagcacgc aagcaactacc aacgagaccc gtcgacgcac acggccgtgc tctacgcggc 3184  
 191 cacccacgtt ctcaactccc ggcactcga cgacaaagac gacccgcgc gctggctcat 3244  
 193 gatcggAACC gacccAGCAG gcccgcctact cgaactcgtc gcaactgtat acgacgacgg 3304  
 195 ctacgaactg atcatccacg caatgaaagc ccgcacccaa tacctcgacc agctctaacc 3364  
 197 aagaaaggaa cctgtatgagc gaccagctag acagcgaccc caactacgac ccgtatgtatct 3424  
 199 tcgacgttatgc gcgcgagacc gccaaccgcg tcgtcgccac gtacgttgca tggaaagatg 3484  
 201 aagccgtatgc tcccccgcgag gtcgcgcact ggcaggccga gcgattccgc accccggcaccg 3544  
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 208 <212> TYPE: PRT  
 209 <213> ORGANISM: Propionibacterium freudenreichii LMG16545  
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 213 1 5 10 15  
 215 Pro Leu Ala Ser Ala Glu Lys Ser Gly Ala Tyr Arg His Val Thr Arg  
 216 20 25 30  
 218 Gln Arg Ala Leu Glu Leu Pro Tyr Ile Glu Ala Asn Pro Leu Val Met  
 219 35 40 45  
 221 Gln Ser Leu Val Ile Thr Asp Arg Asp Ala Ser Asp Ala Asp Trp Ala  
 222 50 55 60  
 224 Ala Asp Leu Ala Gly Leu Pro Ser Pro Ser Tyr Val Ser Met Asn Arg  
 225 65 70 75 80  
 227 Val Thr Thr Thr Gly His Ile Val Tyr Ala Leu Lys Asn Pro Val Cys  
 228 85 90 95  
 230 Leu Thr Asp Ala Ala Arg Arg Arg Pro Ile Asn Leu Leu Ala Arg Val

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231           100          105          110
233 Glu Gln Gly Leu Cys Asp Val Leu Gly Gly Asp Ala Ser Tyr Gly His
234           115          120          125
236 Arg Ile Thr Lys Asn Pro Leu Ser Thr Ala His Ala Thr Leu Trp Gly
237           130          135          140
239 Pro Ala Asp Ala Leu Tyr Glu Leu Arg Ala Leu Ala His Thr Leu Asp
240 145           150          155          160
242 Glu Ile His Ala Leu Pro Glu Ala Gly Asn Pro Arg Arg Asn Val Thr
243           165          170          175
245 Arg Ser Thr Val Gly Arg Asn Val Thr Leu Phe Asp Thr Thr Arg Met
246           180          185          190
248 Trp Ala Tyr Arg Ala Val Arg His Ser Trp Gly Gly Pro Val Ala Glu
249           195          200          205
251 Trp Glu His Thr Val Phe Glu His Ile His Leu Leu Asn Glu Thr Ile
252           210          215          220
254 Ile Ala Asp Glu Phe Ala Thr Gly Pro Leu Gly Leu Asn Glu Leu Lys
255 225           230          235          240
257 His Leu Ser Arg Ser Ile Ser Arg Trp Val Trp Arg Asn Phe Thr Pro
258           245          250          255
260 Glu Thr Phe Arg Ala Arg Gln Lys Ala Ile Ser Leu Arg Gly Ala Ser
261           260          265          270
263 Lys Gly Gly Lys Glu Gly Gly His Lys Gly Gly Ile Ala Ser Gly Ala
264           275          280          285
266 Ser Arg Arg Ala His Thr Arg Gln Gln Phe Leu Glu Gly Leu Ser
267           290          295          300
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271 <211> LENGTH: 85
272 <212> TYPE: PRT
273 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
275 <400> SEQUENCE: 3
276 Met Thr Thr Arg Glu Arg Leu Pro Arg Asn Gly Tyr Ser Ile Ala Ala
277 1           5          10          15
279 Ala Ala Lys Lys Leu Gly Val Ser Glu Ser Thr Val Lys Arg Trp Thr
280           20          25          30
282 Ser Glu Pro Arg Glu Glu Phe Val Ala Arg Val Ala Ala Arg His Ala
283           35          40          45
285 Arg Ile Arg Glu Leu Arg Ser Glu Gly Gln Ser Met Arg Ala Ile Ala
286           50          55          60
288 Ala Glu Val Gly Val Ser Val Gly Thr Val His Tyr Ala Leu Asn Lys
289 65           70          75          80
291 Asn Arg Thr Asp Ala
292           85
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296 <211> LENGTH: 59
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298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvaI
303 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING  
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304 aattcaagct tgtcgacgtt aacctgcagg catgcggatc cggtaccgat atcagatct 59  
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308 <211> LENGTH: 59  
309 <212> TYPE: DNA  
310 <213> ORGANISM: Artificial Sequence  
312 <220> FEATURE:  
313 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvAI  
315 <400> SEQUENCE: 5  
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320 <211> LENGTH: 24  
321 <212> TYPE: DNA  
322 <213> ORGANISM: Artificial Sequence  
324 <220> FEATURE:  
325 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends  
327 <400> SEQUENCE: 6  
328 gtaccggccg ctgcggccaa gctt 24  
331 <210> SEQ ID NO: 7  
332 <211> LENGTH: 24  
333 <212> TYPE: DNA  
334 <213> ORGANISM: Artificial Sequence  
336 <220> FEATURE:  
337 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends  
339 <400> SEQUENCE: 7  
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346 <213> ORGANISM: Artificial Sequence  
348 <220> FEATURE:  
349 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance  
351 <400> SEQUENCE: 8  
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356 <211> LENGTH: 76  
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358 <213> ORGANISM: Artificial Sequence  
360 <220> FEATURE:  
361 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance  
363 <400> SEQUENCE: 9  
364 aaactgcagc agctgggcag gcccgtggac ggcctgcctt cgagctcgtc tagaatgtgc 60  
366 tgccgatctt ggttgc 76  
369 <210> SEQ ID NO: 10  
370 <211> LENGTH: 32  
371 <212> TYPE: DNA  
372 <213> ORGANISM: Artificial Sequence  
374 <220> FEATURE:  
375 <223> OTHER INFORMATION: Synthetic primer for cobA  
377 <400> SEQUENCE: 10

**VERIFICATION SUMMARY**

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Input Set : A:\MBHB00-1314\_SequenceListing.txt

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